



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Cottarel, Guillaume  
Damagnez, Veronique  
Draetta, Guilo
- (ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from  
Human Pathogens, and Uses Related Thereto
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Foley, Hoag & Eliot, LLP
  - (B) STREET: One Post Office Square
  - (C) CITY: Boston
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: ASCII (text)
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 09/072994
  - (B) FILING DATE: 05-MAY-1998
  - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Vincent, Matthew P.
  - (B) REGISTRATION NUMBER: 36,709
  - (C) REFERENCE/DOCKET NUMBER: MIV032.02

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1668 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 259..1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATGATACA AATGTGGAAG ATGCAAATTG TTCTTCCCCT ACTTTGATGA GAAAAAGTGC	60
ATTGAGTAAA ATCATCTTCA AAGGACATTA AACAATAATT CCAAATCACC ATCGCCAAC	120

TTTTCAAATA CAAATGCAAC ATCTGGCTCT CCATTGTCAA ATCTTTCTCG TGCACCATTG	180
AGAAATTTAT CTAATTTTCGT TATTCCTTTCG TCAGTTAAAT CAAAAACGAA ACAATTTACA	240
AACTCTTTGA CTCGTTCA ATG ACT GAA GTG GTT TCG AAA TCA TCA CAC TCA Met Thr Glu Val Val Ser Lys Ser Ser His Ser 1 5 10	291
TTT TTC AAT AAT TTG CAT CTT GCA ACC TCA ACT GCG TCT TCT TCA GTA Phe Phe Asn Asn Leu His Leu Ala Thr Ser Thr Ala Ser Ser Ser Val 15 20 25	339
TCG AGC ACA ACT CCC AAA ATA GAA TTC AAT TCC ATA GCT GAA AAT GAT Ser Ser Thr Thr Pro Lys Ile Glu Phe Asn Ser Ile Ala Glu Asn Asp 30 35 40	387
GAT ATC CCT ACC AAT TAT GAC TCT GAT GAA GAA TTC GAA GAT GGT GAT Asp Ile Pro Thr Asn Tyr Asp Ser Asp Glu Glu Phe Glu Asp Gly Asp 45 50 55	435
ACG TTT ATA CAA TCC ACC TTG ATT CAC CAG TTC AAC GCA AGT CAA GTA Thr Phe Ile Gln Ser Thr Leu Ile His Gln Phe Asn Ala Ser Gln Val 60 65 70 75	483
ACA ACA ACA ACA ATA ATA ATA ATA CCA ATG ATG GTA ACG ACA ATA ATA Thr Thr Thr Thr Ile Ile Ile Ile Pro Met Met Val Thr Thr Ile Ile 80 85 90	531
TAC CTA CAA AAA TTA GAC GGT TCC ACT CCA TGT ACC AAA CCG ATA AAG Tyr Leu Gln Lys Leu Asp Gly Ser Thr Pro Cys Thr Lys Pro Ile Lys 95 100 105	579
AGA TTG CAT CGT ACC AAC TTC ATG AAG ATA ATT CAT TTT GAA ATT TAC Arg Leu His Arg Thr Asn Phe Met Lys Ile Ile His Phe Glu Ile Tyr 110 115 120	627
AAT ATT GAA TAT TCT CAT CTG GAG AGT GAT TTG TTA CCA CGA ATC GAT Asn Ile Glu Tyr Ser His Ser Glu Ser Asp Leu Leu Pro Arg Ile Asp 125 130 135	675
GCT CAT CAA TTA GCC AGA ATA TTA CGT GGA GAC CAC GAT GAC CAA TTT Ala His Gln Leu Ala Arg Ile Leu Arg Gly Asp His Asp Asp Gln Phe 140 145 150 155	723
GAT GAA TTT ATT ATC ATT GAT TGT CGA TTT GAG TAT GAA TTT AAT GGT Asp Glu Phe Ile Ile Ile Asp Cys Arg Phe Glu Tyr Glu Phe Asn Gly 160 165 170	771
GGC CAT ATT ACT AGG GCA ATC AAT ATC TCC ACC CAG GAA GCA CTT CAA Gly His Ile Thr Arg Ala Ile Asn Ile Ser Thr Gln Glu Ala Leu Gln 175 180 185	819
GAA AAG CTC TTT CAA TAT CAA GAA ACA GAT ACC AAG GAC ACT GAA AGC Glu Lys Leu Phe Gln Tyr Gln Glu Thr Asp Thr Lys Asp Thr Glu Ser 190 195 200	867
AAG AAG CGA TTG ATA ATT TTC CAT TGT GAG TTC AGT ATG TTC AGA GGA Lys Lys Arg Leu Ile Ile Phe His Cys Glu Phe Ser Met Phe Arg Gly 205 210 215	915
CCA ATG ATG GCC AAA CAT TTA AGA AAG TGT GAT AGA ATG TGC AAC TAC Pro Met Met Ala Lys His Leu Arg Lys Cys Asp Arg Met Cys Asn Tyr	963

220	225	230	235	
GAC AAT TAT CCT CTA TTA ACA TAC CCC GAT ATT GCA ATT TTG GAA GGA Asp Asn Tyr Pro Leu Leu Thr Tyr Pro Asp Ile Ala Ile Leu Glu Gly 240 245 250				1011
GGC TAT AAG AAT TTC TAT GAA AAT TAC CCC CAA TGG TGT GAT CCT CAA Gly Tyr Lys Asn Phe Tyr Glu Asn Tyr Pro Gln Trp Cys Asp Pro Gln 255 260 265				1059
GGA TAT GTC GAG ATG AAG AAT TTA CGA CAC AAA AAA TTA TGT GAA TCC Gly Tyr Val Glu Met Lys Asn Leu Arg His Lys Lys Leu Cys Glu Ser 270 275 280				1107
AAC TTG GAT AAA GTT AGA AAA GAT AAT AAA CTA ACT AGA GCA AAG TCT Asn Leu Asp Lys Val Arg Lys Asp Asn Lys Leu Thr Arg Ala Lys Ser 285 290 295				1155
TAT CAA TTT GGT ATT CAA CAC CGC CGT GGT GGT TCC ACT GGT GGA CTT Tyr Gln Phe Gly Ile Gln His Arg Arg Gly Gly Ser Thr Gly Gly Leu 300 305 310 315				1203
TTC GGC AAC TAT AAT TAC AAC GTT ATG AAC TCA TCA GAT CAA CAA TTT Phe Gly Asn Tyr Asn Tyr Asn Val Met Asn Ser Ser Asp Gln Gln Phe 320 325 330				1251
TGG AGT AGC AGT ACT TCC AAC ACT GCT CAC CAC AGA AGT AGT AGC AGT Trp Ser Ser Ser Thr Ser Asn Thr Ala His His Arg Ser Ser Ser Ser 335 340 345				1299
AGC GGG TTC ATT AAT AAT ATG CAT AGT GGT GCT TCG TCA TAT CAC CAT Ser Gly Phe Ile Asn Asn Met His Ser Gly Ala Ser Ser Tyr His His 350 355 360				1347
AGG TCA CAA TCG TTT GTA ACT ATC AAT AAT GAG AAA ATT ATC AAG CGA Arg Ser Gln Ser Phe Val Thr Ile Asn Asn Glu Lys Ile Ile Lys Arg 365 370 375				1395
CAA AGA TCG ACT CCC AAA GTC AGC AAC TCA CCA ACC AAG CCA CCT CAT Gln Arg Ser Thr Pro Lys Val Ser Asn Ser Pro Thr Lys Pro Pro His 380 385 390 395				1443
CAA CTG TAT CTC CTG ATA AAC CCA TTC CGT TGG CTA ATA TTC ATA GAT Gln Ser Tyr Leu Ser Ile Asn Pro Phe Arg Trp Leu Ile Phe Ile Asp 400 405 410				1491
TAACTCGTGC CAACACTATT TCATCAGACC AAACATTGTT TAGCAATAAG CTGGTATCTT				1551
CCCCAATGAT ATCTCCACTT GCAGCTAGTT TTGAACAATC GTCGATTGGA ATAAGTTCTT				1611
CTGAATTATC AGTCAATACT CAAGATTTTC AACCACCGAC TACGTCCTTT AGGAATT				1668

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 208..513

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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AACTTGTTTA CTTATTTGTT TATATAATTG ATAGATATCA ATTACTAATT TACCCTTGTT      60
TTTTACTTCC TACTATTCAA GACTTTATTT CCTCCTGATA ATCATTTTGT TTGATTATCA      120
TTTTCGTCAA TTAGTTCTTT TTTTTCATTT GTTCCAGAG TTTAGGAAGA CTACCATTTT      180
ACAATTTTCA ATTCAAATAT TTTCCCA ATG ACT AAA CCA AGA TTT TTA ACA      231
                               Met Thr Lys Pro Arg Phe Leu Thr
                               1                               5

AGA TAT AGA AAG AGC AAA AGT GTT GGA ATT TCA GAT ATG ATC CAT TAC      279
Arg Tyr Arg Lys Ser Lys Ser Val Gly Ile Ser Asp Met Ile His Tyr
   10                               15                               20

AGT CCC AGA TAC AGT GAT GAT TCA TAC GAG TAT AGA CAT GTG ATG TTA      327
Ser Pro Arg Tyr Ser Asp Asp Ser Tyr Glu Tyr Arg His Val Met Leu
   25                               30                               35                               40

CCC AAG AAT ATG TTG AAA GCA ATT CCT CAC GAT TAC TTT AAT CAA GAA      375
Pro Lys Asn Met Leu Lys Ala Ile Pro His Asp Tyr Phe Asn Gln Glu
                               45                               50                               55

ACA GGT ACT TTG AGG ATA TTG ACA GAA GAA GAA TGG AGA GGG TTA GGA      423
Thr Gly Thr Leu Arg Ile Leu Thr Glu Glu Glu Trp Arg Gly Leu Gly
                               60                               65                               70

ATC ACA CAA TCT TTG GGT TGG GCC CAT TAC GAA ACT CAT GCT CCA GAG      471
Ile Thr Gln Ser Leu Gly Trp Ala His Tyr Glu Thr His Ala Pro Glu
   75                               80                               85

CCT CAT ATA TTA TTA TTC AAG AGA CCC TTA AAT CCC GGG CAA      513
Pro His Ile Leu Leu Phe Lys Arg Pro Leu Asn Pro Gly Gln
   90                               95                               100

TAAAAAGATT AACTATATTT GAATACTATA GAATCGGAAT CGGTTTTTAAA GTTAACACTG      573
GAATTAAAAC ATAAAAAGGA AAGAAATAGC CCATTGGTCA CAGTAATCTG TTTCCAACAA      633
CCCCCCTCCT CAGAAATAGG ATAGAAATGA ATTAACGATG AATTTGTATA CACTATTTAT      693
AAGCCAATCT CATTGATTGC ATTTCTTATT TGTATATTAT TAAATACGTA TATCGCGAGA      753
AACTGTATAA ATACTCTTGG TACCTCGCAT GTT      786

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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 43..993

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TAGAACACAC ACATCCCAAG CCAAGACCAA CACTTATTGC	AA ATG GTA GAG TTA	54
	Met Val Glu Leu	
	1	
TCT GAT TAT CAA CGT CAA GAA AAA GTC GGA GAA GGT ACT TAT GGG GTT	102	
Ser Asp Tyr Gln Arg Gln Glu Lys Val Gly Glu Gly Thr Tyr Gly Val		
5 10 15 20		
GTT TAT AAA GCA TTA GAT ACC AAG CAC AAT AAT AGA GTT GTT GCA TTA	150	
Val Tyr Lys Ala Leu Asp Thr Lys His Asn Asn Arg Val Val Ala Leu		
25 30 35		
AAG AAA ATT CGA TTA GAA TCA GAA GAT GAA GGT GTA CCT AGT ACC GCC	198	
Lys Lys Ile Arg Leu Glu Ser Glu Asp Glu Gly Val Pro Ser Thr Ala		
40 45 50		
ATT AGA GAA ATC TCG TTA TTA AAA GAA ATG AAA GAT GAT AAT ATC GTT	246	
Ile Arg Glu Ile Ser Leu Leu Lys Glu Met Lys Asp Asp Asn Ile Val		
55 60 65		
CGA TTA TAT GAT ATT ATT CAT TCA GAT TCT CAT AAA TTA TAT TTA GTA	294	
Arg Leu Tyr Asp Ile Ile His Ser Asp Ser His Lys Leu Tyr Leu Val		
70 75 80		
TTT GAA TTT TTG GAT TTA GAT TTA AAG AAA TAT ATG GAA AGT ATT CCT	342	
Phe Glu Phe Leu Asp Leu Asp Leu Lys Lys Tyr Met Glu Ser Ile Pro		
85 90 95 100		
CAA GGA GTT GGA CTA GGG GCT AAT ATG ATA AAA AGA TTT ATG AAT CAA	390	
Gln Gly Val Gly Leu Gly Ala Asn Met Ile Lys Arg Phe Met Asn Gln		
105 110 115		
TTA ATT CGA GGT ATT AAA CAT TGT CAT TCT CAT CGA GTT TTA CAT CGT	438	
Leu Ile Arg Gly Ile Lys His Cys His Ser His Arg Val Leu His Arg		
120 125 130		
GAT TTA AAA CCA CAA AAT TTA TTG ATT GAT AAA GAA GGG AAT TTA AAA	486	
Asp Leu Lys Pro Gln Asn Leu Leu Ile Asp Lys Glu Gly Asn Leu Lys		
135 140 145		
TTA GCA GAT TTT GGA TTA GCT CGA GCA TTT GGA GTT CCA TTA AGA GCA	534	
Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Leu Arg Ala		
150 155 160		
TAT ACT CAT GAA GTT GTC ACT TTA TGG TAT CGA GCT CCC GAA ATC TTG	582	
Tyr Thr His Glu Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Ile Leu		
165 170 175 180		
TTA GGA GGG AAA CAA TAT TCC ACT GGG GTA GAT ATG TGG TCT GTT GGA	630	
Leu Gly Gly Lys Gln Tyr Ser Thr Gly Val Asp Met Trp Ser Val Gly		
185 190 195		
TGT ATA TTT GCT GAA ATG TGT AAT AGG AAA CCA TTA TTT CCT GGT GAT	678	
Cys Ile Phe Ala Glu Met Cys Asn Arg Lys Pro Leu Phe Pro Gly Asp		

200	205	210	
TCA GAA ATT GAT GAA ATT TTC CGA ATT TTC CGA ATT TTA GGA ACA CCT Ser Glu Ile Asp Glu Ile Phe Arg Ile Phe Arg Ile Leu Gly Thr Pro 215 220 225			726
AAT GAA GAA ATT TGG CCT GAT GTT AAT TAT TTA CCA GAT TTT AAA TCA Asn Glu Glu Ile Trp Pro Asp Val Asn Tyr Leu Pro Asp Phe Lys Ser 230 235 240			774
AGT TTC CCT CAA TGG AAA AAG AAA CCT TTG AGT GAA GCA GTT CCA AGT Ser Phe Pro Gln Trp Lys Lys Lys Pro Leu Ser Glu Ala Val Pro Ser 245 250 255 260			822
TTG GAT GCT AAT GGA ATT GAT CTT TTG GAT CAA ATG TTG GTG TAT GAT Leu Asp Ala Asn Gly Ile Asp Leu Leu Asp Gln Met Leu Val Tyr Asp 265 270 275			870
CCA AGT AGA AGA ATA AGT GCT AAA CGA GCT TTA ATT CAT CCT TAT TTT Pro Ser Arg Arg Ile Ser Ala Lys Arg Ala Leu Ile His Pro Tyr Phe 280 285 290			918
AAT GAT AAT GAT GAT CGT GAT CAT AAC AAT TAT AAT GAA GAT AAT ATT Asn Asp Asn Asp Asp Arg Asp His Asn Asn Tyr Asn Glu Asp Asn Ile 295 300 305			966
GGG ATT GAC AAA CAC CAA AAC ATG CAA TAAATCTTG Gly Ile Asp Lys His Gln Asn Met Gln 310 315			1002

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 184..1659

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTATTCCCC CCTTTTCCTT TTTTTTATAG AGAAACTTAT TCCAATTACT CATCGAACAA	60
GATCTTACTA GACTTGTAGA CTCACGACAC GATAAATTTT AATTCATTAA TCAACCAACG	120
AACCAGCCAA ACCAAAATTA ATTCACATTT ATACTCACTG TTTGTCATTT TCATCTCATA	180
GTA ATG CCA CAA GTC ACT AAA ACT AAT AAT GAA AAT GAG TTT AGA CTT Met Pro Gln Val Thr Lys Thr Asn Asn Glu Asn Glu Phe Arg Leu 1 5 10 15	228
ACT AGA TCA AAA GTA CAG CAT CAA GAG TCG ATA AGT ACC ATC AAA AAT Thr Arg Ser Lys Val Gln His Gln Glu Ser Ile Ser Thr Ile Lys Asn 20 25 30	276

ACG	ACC	ATA	TCC	AAT	TCT	CAG	CAT	AAA	CAA	CAA	ACA	CAA	CAA	CAA	ATT	324
Thr	Thr	Ile	Ser	Asn	Ser	Gln	His	Lys	Gln	Gln	Thr	Gln	Gln	Gln	Ile	
			35					40					45			
TCA	TCA	CCA	CCT	CAA	GTC	TCT	GTA	ACA	TCA	TCT	GAA	GGA	GTT	TCA	CAT	372
Ser	Ser	Pro	Pro	Gln	Val	Ser	Val	Thr	Ser	Ser	Glu	Gly	Val	Ser	His	
		50					55					60				
GTC	AAT	ACA	CGT	CAA	TAT	TTG	GGT	GAT	GTT	TCA	AAT	CAA	TAC	ATA	ACA	420
Val	Asn	Thr	Arg	Gln	Tyr	Leu	Gly	Asp	Val	Ser	Asn	Gln	Tyr	Ile	Thr	
	65					70					75					
AAT	GCT	AAA	CCA	ACA	AAT	AAA	AGA	AAA	CCA	TTG	GGT	GGA	GAC	AAT	GCC	468
Asn	Ala	Lys	Pro	Thr	Asn	Lys	Arg	Lys	Pro	Leu	Gly	Gly	Asp	Asn	Ala	
80					85					90					95	
CCT	CTA	CAA	AAA	CAA	CAG	CAT	AGA	CCA	TCT	AGA	CCA	ATA	CCC	ATT	GCC	516
Pro	Leu	Gln	Lys	Gln	Gln	His	Arg	Pro	Ser	Arg	Pro	Ile	Pro	Ile	Ala	
				100					105					110		
AGT	GAT	AAC	AAC	AAT	AAT	GGT	AGT	ACC	AGT	AGC	AGT	AGC	AAC	AGT	AGC	564
Ser	Asp	Asn	Asn	Asn	Asn	Gly	Ser	Thr	Ser	Ser	Ser	Ser	Asn	Ser	Ser	
			115					120					125			
AAC	AAC	AAT	AAC	AAC	GAC	GCA	AAT	AGA	CTA	GCA	TCT	TTG	GCA	GTT	CCA	612
Asn	Asn	Asn	Asn	Asn	Asp	Ala	Asn	Arg	Leu	Ala	Ser	Leu	Ala	Val	Pro	
		130					135					140				
TCT	CGA	TTA	CCC	CAA	AAA	CGA	CAA	GCT	ACT	GAA	TCG	TCG	ACA	AAT	TTA	660
Ser	Arg	Leu	Pro	Gln	Lys	Arg	Gln	Ala	Thr	Glu	Ser	Ser	Thr	Asn	Leu	
	145					150					155					
GTA	GAG	AAA	TTA	AGA	GTA	CCA	CAA	CCA	GAA	GTA	GGG	GAA	AGA	AGT	CAG	708
Val	Glu	Lys	Leu	Arg	Val	Pro	Gln	Pro	Glu	Val	Gly	Glu	Arg	Ser	Gln	
160					165				170						175	
TCA	TAC	CAT	AAG	AAA	TCA	CGT	TTA	ATT	GAT	TAT	GAA	TGG	CAG	GAT	TTG	756
Ser	Tyr	His	Lys	Lys	Ser	Arg	Leu	Ile	Asp	Tyr	Glu	Trp	Gln	Asp	Leu	
				180				185					190			
GAT	GAA	GAA	GAT	AAT	GAC	GAC	CAA	TTA	ATG	GTT	AGT	GAA	TAT	GTT	AAC	804
Asp	Glu	Glu	Asp	Asn	Asp	Asp	Gln	Leu	Met	Val	Ser	Glu	Tyr	Val	Asn	
			195					200					205			
GAA	ATA	TTT	TCG	TAC	TAT	TAC	GAA	TTA	GAA	ACA	CGA	ATG	TTA	CCT	GAT	852
Glu	Ile	Phe	Ser	Tyr	Tyr	Tyr	Glu	Leu	Glu	Thr	Arg	Met	Leu	Pro	Asp	
		210					215					220				
CCG	CAA	TAT	CTT	TTC	AAA	CAA	ACA	TTG	TTA	AAA	CCA	AGA	ATG	AGA	TCG	900
Pro	Gln	Tyr	Leu	Phe	Lys	Gln	Thr	Leu	Leu	Lys	Pro	Arg	Met	Arg	Ser	
		225				230					235					
ATA	TTG	GTT	GAT	TGG	CTT	GTT	GAA	ATG	CAT	TTA	AAA	TTC	AAG	TTA	TTA	948
Ile	Leu	Val	Asp	Trp	Leu	Val	Glu	Met	His	Leu	Lys	Phe	Lys	Leu	Leu	
240				245				250							255	
CCT	GAA	TCA	CTT	TTT	TTG	GCA	GTC	AAT	GTA	ATG	GAT	AGA	TTC	ATG	TCT	996
Pro	Glu	Ser	Leu	Phe	Leu	Ala	Val	Asn	Val	Met	Asp	Arg	Phe	Met	Ser	
				260				265					270			
GTT	GAA	GTG	GTT	CAA	ATA	GAT	AAA	TTA	CAA	TTA	TTG	GCT	ACA	GCA	GCT	1044
Val	Glu	Val	Val	Gln	Ile	Asp	Lys	Leu	Gln	Leu	Leu	Ala	Thr	Ala	Ala	

275						280						285						
TTA	TTT	ACT	GCT	GCC	AAA	AAT	GAA	GAA	GTA	TTT	TCT	CCC	CTG	GTT	AAA			1092
Leu	Phe	Thr	Ala	Ala	Lys	Asn	Glu	Glu	Val	Phe	Ser	Pro	Ser	Val	Lys			
		290					295					300						
AAT	TAT	GCA	TAT	TTC	ACT	GAT	GGT	TCA	TAT	ACT	CCA	GAA	GAA	GTG	GTA			1140
Asn	Tyr	Ala	Tyr	Phe	Thr	Asp	Gly	Ser	Tyr	Thr	Pro	Glu	Glu	Val	Val			
	305					310					315							
CAA	GCA	GAA	AAA	TAC	ATG	CTT	ACC	ATT	CTT	AAC	TTT	GAT	TTG	AAT	TAC			1188
Gln	Ala	Glu	Lys	Tyr	Met	Leu	Thr	Ile	Leu	Asn	Phe	Asp	Leu	Asn	Tyr			
	320				325					330					335			
CCC	AAT	CCA	ATG	AAT	TTC	TTG	AGA	AGA	ATT	TCT	AAA	GCT	GAT	GAT	TAT			1236
Pro	Asn	Pro	Met	Asn	Phe	Leu	Arg	Arg	Ile	Ser	Lys	Ala	Asp	Asp	Tyr			
				340					345					350				
GAT	GTC	CAA	TCA	AGA	ACG	CTA	GGA	AAA	TAT	CTT	TTG	GAA	ATC	ACT	ATA			1284
Asp	Val	Gln	Ser	Arg	Thr	Leu	Gly	Lys	Tyr	Leu	Leu	Glu	Ile	Thr	Ile			
			355				360						365					
GTT	GAT	TAC	AAA	TTT	ATT	GGT	ATG	AGA	CCA	TCT	TTA	TGT	TGT	GCC	CTG			1332
Val	Asp	Tyr	Lys	Phe	Ile	Gly	Met	Arg	Pro	Ser	Leu	Cys	Cys	Ala	Ser			
		370				375						380						
GCC	ATG	TAT	TTA	GCA	AGA	CTA	ATA	TTG	GGC	AAA	TTG	CCA	GTT	TGG	AAT			1380
Ala	Met	Tyr	Leu	Ala	Arg	Leu	Ile	Leu	Gly	Lys	Leu	Pro	Val	Trp	Asn			
	385					390					395							
GGG	AAT	TTG	ATT	CAT	TAT	AGT	GGA	GGT	TAT	AGA	ATC	AGT	GAT	ATG	AGA			1428
Gly	Asn	Leu	Ile	His	Tyr	Ser	Gly	Gly	Tyr	Arg	Ile	Ser	Asp	Met	Arg			
	400				405					410					415			
GAA	TGT	ATC	GAA	TTA	ATG	TTT	CAA	TAT	CTT	ATT	GCT	CCT	ATA	GAA	CAT			1476
Glu	Cys	Ile	Glu	Leu	Met	Phe	Gln	Tyr	Leu	Ile	Ala	Pro	Ile	Glu	His			
				420					425					430				
GAT	GAA	TTT	TTC	AAA	AAA	TAT	GCC	ATG	AGA	AAA	TTT	ATG	AGA	GCA	AGT			1524
Asp	Glu	Phe	Phe	Lys	Lys	Tyr	Ala	Met	Arg	Lys	Phe	Met	Arg	Ala	Ser			
			435				440					445						
ACT	CTT	TGT	CGA	AAT	TGG	GCT	AAA	AAA	TTC	CAA	GCA	TCA	GGA	AGA	GAT			1572
Thr	Leu	Cys	Arg	Asn	Trp	Ala	Lys	Lys	Phe	Gln	Ala	Ser	Gly	Arg	Asp			
		450				455						460						
TTG	TTT	GAT	GAA	CGA	TTA	TCG	ACC	CAT	AGG	CTA	ACA	TTA	GAA	GAT	GAT			1620
Leu	Phe	Asp	Glu	Arg	Leu	Ser	Thr	His	Arg	Leu	Thr	Leu	Glu	Asp	Asp			
	465					470				475								
GAC	GAA	GAA	GAA	GAA	ATA	GTG	GTA	GCA	GAA	GCA	GAA	GAG	TAAAGTTTTG					1669
Asp	Glu	Glu	Glu	Glu	Ile	Val	Val	Ala	Glu	Ala	Glu	Glu						
	480				485					490								
AGGACTATTG GATCTAGGTT CTTATCTTTA CAATGCATAA ATGAGGAAAT GAAAGAAGAT																		1729
GAACATGAGT TATGTGCATT ACC																		1752

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1070 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 30..1058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATCAAATCCA TCAGAGAACC ACATCAATC	ATG TCT ACT GCA GCA GTT GCA ACG	53
	Met Ser Thr Ala Ala Val Ala Thr	
	1 5	
AAA CCA TCT GTC ACT TCA AAA CCA GCA ACT AAA CAA GTT CTG AAT TAC	101	
Lys Pro Ser Val Thr Ser Lys Pro Ala Thr Lys Gln Val Leu Asn Tyr		
	10 15 20	
ACC AAA GAA AAA AAA GTA GGG GAA GGT ACA TAT GCT GTT GTG TAC TTG	149	
Thr Lys Glu Lys Lys Val Gly Glu Gly Thr Tyr Ala Val Val Tyr Leu		
	25 30 35 40	
GGT AAA CAA ATC TCC ACC AAA CGT CAA ATT GCC ATC AAA GAA ATC AAA	197	
Gly Lys Gln Ile Ser Thr Lys Arg Gln Ile Ala Ile Lys Glu Ile Lys		
	45 50 55	
ACA GGA TTA TTC AAA GAT GGG TTG GAT ATG TCA GCA TTG AGA GAA GTG	245	
Thr Gly Leu Phe Lys Asp Gly Leu Asp Met Ser Ala Leu Arg Glu Val		
	60 65 70	
AAA TAT TTG CAA GAA TTG AAA CAT CCC AAT GTT ATT GAA CTA GTA GAT	293	
Lys Tyr Leu Gln Glu Leu Lys His Pro Asn Val Ile Glu Leu Val Asp		
	75 80 85	
GTA TTT TCA GCA ACA AAT AAT TTA AAT TTG GTA TTA GAA TTT CTA CCT	341	
Val Phe Ser Ala Thr Asn Asn Leu Asn Leu Val Leu Glu Phe Leu Pro		
	90 95 100	
TGC GAT TTG GAA GTG TTG ATC AAA GAT AAA TCG ATT GTT TTC AAA TCA	389	
Cys Asp Leu Glu Val Leu Ile Lys Asp Lys Ser Ile Val Phe Lys Ser		
	105 110 115 120	
GCA GAT ATC AAA TCA TGG CTT TTA ATG ACA TTA CGT GGG ATA CAT CAT	437	
Ala Asp Ile Lys Ser Trp Leu Leu Met Thr Leu Arg Gly Ile His His		
	125 130 135	
TGT CAT CGG AAT TTT ATT TTA CAT CGT GAT TTG AAA CCA AAT AAT TTA	485	
Cys His Arg Asn Phe Ile Leu His Arg Asp Leu Lys Pro Asn Asn Leu		
	140 145 150	
TTA TTG GCA CCG GAT GGA CAA TTG AAA ATA GCG GAT TTT GGT CTT GCA	533	
Leu Leu Ala Pro Asp Gly Gln Leu Lys Ile Ala Asp Phe Gly Leu Ala		
	155 160 165	
CGA GCT TTG GTA AAT CCT AAT GAA GAT TTA TCA TCT AAT GTT GTC ACT	581	
Arg Ala Leu Val Asn Pro Asn Glu Asp Leu Ser Ser Asn Val Val Thr		

170	175	180	
AGA TGG TAT AGA GCC CCT GAA TTA TTA TTT GGT GCT CGA CAT TAC ACT			629
Arg Trp Tyr Arg Ala Pro Glu Leu Leu Phe Gly Ala Arg His Tyr Thr			
185	190	195	200
GGA GCA GTT GAT ATC TGG TCA ATA GGT ATA ATA TTT GCT GAA TTA ATG			677
Gly Ala Val Asp Ile Trp Ser Ile Gly Ile Ile Phe Ala Glu Leu Met			
	205	210	215
CTT CGA ATA CCT TAT TTG CCA GGT AAA GAT GAC GTT GAT CAA TTA GAT			725
Leu Arg Ile Pro Tyr Leu Pro Gly Lys Asp Asp Val Asp Gln Leu Asp			
	220	225	230
GTT ACA TTT AGA GCT TAT GGG ACA CCA ACA GAG CAA ATA TGG CCA AAT			773
Val Thr Phe Arg Ala Tyr Gly Thr Pro Thr Glu Gln Ile Trp Pro Asn			
	235	240	245
GTT TCC AGT TTG CCA ATG TAT AAT GCA CTT CAT GTG TAT CCA CCT CCT			821
Val Ser Ser Leu Pro Met Tyr Asn Ala Leu His Val Tyr Pro Pro Pro			
	250	255	260
TCA AGA CAA GAA TTA CGT AAT AGA TTT AGT GCT GCT ACG GAA AAA GCC			869
Ser Arg Gln Glu Leu Arg Asn Arg Phe Ser Ala Ala Thr Glu Lys Ala			
265	270	275	280
CTT GAT TTG TTG ATA TCG ATG ACC CAA TTG GAT CCA AGT AGA AGA TGT			917
Leu Asp Leu Leu Ile Ser Met Thr Gln Leu Asp Pro Ser Arg Arg Cys			
	285	290	295
GAT TCT ACA CTA GCA TTA TTA CAC GAT TAT TTT ACT GAA TCG CCT CGT			965
Asp Ser Thr Leu Ala Leu Leu His Asp Tyr Phe Thr Glu Ser Pro Arg			
	300	305	310
CCT ACT GAC CCG AAA AAG TTG CCT AAA AAG TCT TCT CCA GAA AAG AGA			1013
Pro Thr Asp Pro Lys Lys Leu Pro Lys Lys Ser Ser Pro Glu Lys Arg			
	315	320	325
GAA AAT GAA GAT GAA CAG AAT AAT GGC TCT AAA AGA AGG CAT GTT			1058
Glu Asn Glu Asp Glu Gln Asn Asn Gly Ser Lys Arg Arg His Val			
330	335	340	
TAGGTTTCTA TA			1070

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..477

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGT Cys 1	TCA Ser	GCT Ala	ATT Ile	GAT Asp 5	ACG Thr	AAA Lys	AGT Ser	TCA Ser	GTC Val 10	TCA Ser	GCG Ala	ATG Met	GAG Glu	CAC His 15	AAG Lys	48
ATT Ile	GCT Ala	ATA Ile	AAG Lys 20	AAA Lys	GTA Val	ACA Thr	AAG Lys	ATT Ile 25	TTC Phe	AAC Asn	AAA Lys	GAC Asp	ATC Ile 30	CTT Leu	CTA Leu	96
ATC Ile	AGG Arg	GCA Ala 35	ATA Ile	CGA Arg	GAG Glu	CTT Leu	AAG Lys 40	TTC Phe	ATG Met	ATG Met	TTT Phe	TTC Phe 45	AGA Arg	GGC Gly	CAC His	144
AAG Lys 50	AAT Asn	ATT Ile	GCA Ala	ACT Thr	TTG Leu	CTT Leu 55	GAC Asp	TTA Leu	GAT Asp	GTT Val 60	GTA Val	TAT Tyr	GTG Val	AAG Lys	CCT Pro	192
TAT Tyr 65	GAA Glu	GGC Gly	TTG Leu	TAT Tyr	TGT Cys 70	TTT Phe	CAA Gln	GAG Glu	CTA Leu	GCC Ala 75	GAT Asp	TTA Leu	GAT Asp	TTA Leu	GCT Ala 80	240
CGT Arg	GTT Val	TTG Leu	TAC Tyr	TCA Ser 85	AAC Asn	GTC Val	CAA Gln	TTT Phe 90	TCA Ser	GAA Glu	TTT Phe	CAC His	ATT Ile	CAA Gln 95	AGC Ser	288
TTT Phe	ATG Met	TAC Tyr	CAA Gln 100	ATT Ile	CTT Leu	TGC Cys	GGA Gly	CTC Leu 105	AAG Lys	TAC Tyr	ATC Ile	CAT His	TCT Ser 110	GCT Ala	GAT Asp	336
GTA Val	ATA Ile	CAT His 115	CGG Arg	GAC Asp	CTA Leu	AAG Lys	CCA Pro	GGA Gly	AAC Asn	ATA Ile	TTG Leu	GTC Val 125	ACC Thr	ACT Thr	CAA Gln	384
GGG Gly 130	ACT Thr	TTA Leu	AAA Lys	ATA Ile	TGT Cys	GAT Asp 135	TTC Phe	GGC Gly	TTA Leu	GCA Ala	CGA Arg 140	GGA Gly	ATA Ile	AAT Asn	CCT Pro	432
GTA Val 145	TAT Tyr	TTC Phe	AGA Arg	AAC Asn	CGC Arg 150	TCA Ser	GCT Ala	GTC Val	ATC Ile	ACA Thr 155	AAC Asn	TAC Tyr	GTA Val	GCA Ala		477

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met 1	Thr	Glu	Val	Val 5	Ser	Lys	Ser	Ser	His 10	Ser	Phe	Phe	Asn	Asn 15	Leu
His	Leu	Ala	Thr	Ser	Thr	Ala	Ser	Ser 25	Ser	Val	Ser	Ser	Thr 30	Thr	Pro
Lys	Ile	Glu	Phe	Asn	Ser	Ile	Ala	Glu	Asn	Asp	Asp	Ile 45	Pro	Thr	Asn
Tyr	Asp	Ser	Asp	Glu	Glu	Phe	Glu	Asp	Gly	Asp	Thr	Phe	Ile	Gln	Ser

50					55					60					
Thr 65	Leu	Ile	His	Gln	Phe 70	Asn	Ala	Ser	Gln	Val 75	Thr	Thr	Thr	Thr	Ile 80
Ile	Ile	Ile	Pro	Met 85	Met	Val	Thr	Thr	Ile 90	Ile	Tyr	Leu	Gln	Lys 95	Leu
Asp	Gly	Ser	Thr 100	Pro	Cys	Thr	Lys	Pro 105	Ile	Lys	Arg	Leu	His 110	Arg	Thr
Asn	Phe 115	Met	Lys	Ile	Ile	His	Phe 120	Glu	Ile	Tyr	Asn 125	Ile	Glu	Tyr	Ser
His 130	Leu	Glu	Ser	Asp	Leu	Leu 135	Pro	Arg	Ile	Asp	Ala 140	His	Gln	Leu	Ala
Arg 145	Ile	Leu	Arg	Gly	Asp 150	His	Asp	Asp	Gln	Phe 155	Asp	Glu	Phe	Ile	Ile 160
Ile	Asp	Cys	Arg	Phe 165	Glu	Tyr	Glu	Phe	Asn 170	Gly	Gly	His	Ile	Thr 175	Arg
Ala	Ile	Asn 180	Ile	Ser	Thr	Gln	Glu	Ala 185	Leu	Gln	Glu	Lys	Leu 190	Phe	Gln
Tyr	Gln 195	Glu	Thr	Asp	Thr	Lys	Asp 200	Thr	Glu	Ser	Lys	Lys 205	Arg	Leu	Ile
Ile 210	Phe	His	Cys	Glu	Phe	Ser 215	Met	Phe	Arg	Gly	Pro 220	Met	Met	Ala	Lys
His 225	Leu	Arg	Lys	Cys	Asp 230	Arg	Met	Cys	Asn 235	Tyr	Asp	Asn	Tyr	Pro	Leu 240
Leu	Thr	Tyr	Pro	Asp 245	Ile	Ala	Ile	Leu	Glu 250	Gly	Gly	Tyr	Lys	Asn 255	Phe
Tyr	Glu	Asn 260	Tyr	Pro	Gln	Trp	Cys	Asp 265	Pro	Gln	Gly	Tyr	Val 270	Glu	Met
Lys	Asn 275	Leu	Arg	His	Lys	Lys	Leu 280	Cys	Glu	Ser	Asn 285	Leu	Asp	Lys	Val
Arg 290	Lys	Asp	Asn	Lys	Leu	Thr 295	Arg	Ala	Lys	Ser	Tyr 300	Gln	Phe	Gly	Ile
Gln 305	His	Arg	Arg	Gly	Gly 310	Ser	Thr	Gly	Gly	Leu 315	Phe	Gly	Asn	Tyr	Asn 320
Tyr	Asn	Val	Met	Asn 325	Ser	Ser	Asp	Gln	Gln 330	Phe	Trp	Ser	Ser	Ser 335	Thr
Ser	Asn	Thr 340	Ala	His	His	Arg	Ser	Ser 345	Ser	Ser	Ser	Gly	Phe 350	Ile	Asn
Asn	Met 355	His	Ser	Gly	Ala	Ser	Ser 360	Tyr	His	His	Arg	Ser 365	Gln	Ser	Phe
Val 370	Thr	Ile	Asn	Asn	Glu	Lys 375	Ile	Ile	Lys	Arg	Gln 380	Arg	Ser	Thr	Pro

Lys Val Ser Asn Ser Pro Thr Lys Pro Pro His Gln Leu Tyr Leu Leu  
 385 390 395 400

Ile Asn Pro Phe Arg Trp Leu Ile Phe Ile Asp  
 405 410

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Lys Pro Arg Phe Leu Thr Arg Tyr Arg Lys Ser Lys Ser Val  
 1 5 10 15

Gly Ile Ser Asp Met Ile His Tyr Ser Pro Arg Tyr Ser Asp Asp Ser  
 20 25 30

Tyr Glu Tyr Arg His Val Met Leu Pro Lys Asn Met Leu Lys Ala Ile  
 35 40 45

Pro His Asp Tyr Phe Asn Gln Glu Thr Gly Thr Leu Arg Ile Leu Thr  
 50 55 60

Glu Glu Glu Trp Arg Gly Leu Gly Ile Thr Gln Ser Leu Gly Trp Ala  
 65 70 75 80

His Tyr Glu Thr His Ala Pro Glu Pro His Ile Leu Leu Phe Lys Arg  
 85 90 95

Pro Leu Asn Pro Gly Gln  
 100

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 317 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Val Glu Leu Ser Asp Tyr Gln Arg Gln Glu Lys Val Gly Glu Gly  
 1 5 10 15

Thr Tyr Gly Val Val Tyr Lys Ala Leu Asp Thr Lys His Asn Asn Arg  
 20 25 30

Val Val Ala Leu Lys Lys Ile Arg Leu Glu Ser Glu Asp Glu Gly Val  
 35 40 45

Pro Ser Thr Ala Ile Arg Glu Ile Ser Leu Leu Lys Glu Met Lys Asp  
 50 55 60

Asp 65	Asn	Ile	Val	Arg	Leu 70	Tyr	Asp	Ile	Ile	His 75	Ser	Asp	Ser	His	Lys 80
Leu	Tyr	Leu	Val	Phe 85	Glu	Phe	Leu	Asp	Leu 90	Asp	Leu	Lys	Lys	Tyr 95	Met
Glu	Ser	Ile	Pro 100	Gln	Gly	Val	Gly	Leu 105	Gly	Ala	Asn	Met	Ile 110	Lys	Arg
Phe	Met	Asn 115	Gln	Leu	Ile	Arg	Gly 120	Ile	Lys	His	Cys	His 125	Ser	His	Arg
Val 130	Leu	His	Arg	Asp	Leu	Lys 135	Pro	Gln	Asn	Leu	Leu 140	Ile	Asp	Lys	Glu
Gly 145	Asn	Leu	Lys	Leu	Ala 150	Asp	Phe	Gly	Leu	Ala 155	Arg	Ala	Phe	Gly	Val 160
Pro	Leu	Arg	Ala	Tyr 165	Thr	His	Glu	Val	Val 170	Thr	Leu	Trp	Tyr	Arg 175	Ala
Pro	Glu	Ile	Leu 180	Leu	Gly	Gly	Lys	Gln 185	Tyr	Ser	Thr	Gly	Val 190	Asp	Met
Trp	Ser	Val 195	Gly	Cys	Ile	Phe	Ala 200	Glu	Met	Cys	Asn 205	Arg	Lys	Pro	Leu
Phe 210	Pro	Gly	Asp	Ser	Glu	Ile 215	Asp	Glu	Ile	Phe	Arg 220	Ile	Phe	Arg	Ile
Leu 225	Gly	Thr	Pro	Asn	Glu 230	Glu	Ile	Trp	Pro	Asp 235	Val	Asn	Tyr	Leu	Pro 240
Asp	Phe	Lys	Ser	Ser 245	Phe	Pro	Gln	Trp	Lys 250	Lys	Lys	Pro	Leu	Ser 255	Glu
Ala	Val	Pro	Ser 260	Leu	Asp	Ala	Asn	Gly 265	Ile	Asp	Leu	Leu	Asp 270	Gln	Met
Leu	Val	Tyr 275	Asp	Pro	Ser	Arg	Arg 280	Ile	Ser	Ala	Lys	Arg 285	Ala	Leu	Ile
His 290	Pro	Tyr	Phe	Asn	Asp	Asn 295	Asp	Asp	Arg	Asp	His 300	Asn	Asn	Tyr	Asn
Glu 305	Asp	Asn	Ile	Gly	Ile 310	Asp	Lys	His	Gln	Asn 315	Met	Gln			

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met 1	Pro	Gln	Val	Thr 5	Lys	Thr	Asn	Asn	Glu 10	Asn	Glu	Phe	Arg	Leu 15	Thr
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Arg	Ser	Lys	Val	Gln	His	Gln	Glu	Ser	Ile	Ser	Thr	Ile	Lys	Asn	Thr	20	25	30
Thr	Ile	Ser	Asn	Ser	Gln	His	Lys	Gln	Gln	Thr	Gln	Gln	Gln	Ile	Ser	35	40	45
Ser	Pro	Pro	Gln	Val	Ser	Val	Thr	Ser	Ser	Glu	Gly	Val	Ser	His	Val	50	55	60
Asn	Thr	Arg	Gln	Tyr	Leu	Gly	Asp	Val	Ser	Asn	Gln	Tyr	Ile	Thr	Asn	65	70	75
Ala	Lys	Pro	Thr	Asn	Lys	Arg	Lys	Pro	Leu	Gly	Gly	Asp	Asn	Ala	Pro	85	90	95
Leu	Gln	Lys	Gln	Gln	His	Arg	Pro	Ser	Arg	Pro	Ile	Pro	Ile	Ala	Ser	100	105	110
Asp	Asn	Asn	Asn	Asn	Gly	Ser	Thr	Ser	Ser	Ser	Ser	Asn	Ser	Ser	Asn	115	120	125
Asn	Asn	Asn	Asn	Asp	Ala	Asn	Arg	Leu	Ala	Ser	Leu	Ala	Val	Pro	Ser	130	135	140
Arg	Leu	Pro	Gln	Lys	Arg	Gln	Ala	Thr	Glu	Ser	Ser	Thr	Asn	Leu	Val	145	150	155
Glu	Lys	Leu	Arg	Val	Pro	Gln	Pro	Glu	Val	Gly	Glu	Arg	Ser	Gln	Ser	165	170	175
Tyr	His	Lys	Lys	Ser	Arg	Leu	Ile	Asp	Tyr	Glu	Trp	Gln	Asp	Leu	Asp	180	185	190
Glu	Glu	Asp	Asn	Asp	Asp	Gln	Leu	Met	Val	Ser	Glu	Tyr	Val	Asn	Glu	195	200	205
Ile	Phe	Ser	Tyr	Tyr	Tyr	Glu	Leu	Glu	Thr	Arg	Met	Leu	Pro	Asp	Pro	210	215	220
Gln	Tyr	Leu	Phe	Lys	Gln	Thr	Leu	Leu	Lys	Pro	Arg	Met	Arg	Ser	Ile	225	230	235
Leu	Val	Asp	Trp	Leu	Val	Glu	Met	His	Leu	Lys	Phe	Lys	Leu	Leu	Pro	245	250	255
Glu	Ser	Leu	Phe	Leu	Ala	Val	Asn	Val	Met	Asp	Arg	Phe	Met	Ser	Val	260	265	270
Glu	Val	Val	Gln	Ile	Asp	Lys	Leu	Gln	Leu	Leu	Ala	Thr	Ala	Ala	Leu	275	280	285
Phe	Thr	Ala	Ala	Lys	Asn	Glu	Glu	Val	Phe	Ser	Pro	Leu	Val	Lys	Asn	290	295	300
Tyr	Ala	Tyr	Phe	Thr	Asp	Gly	Ser	Tyr	Thr	Pro	Glu	Glu	Val	Val	Gln	305	310	315
Ala	Glu	Lys	Tyr	Met	Leu	Thr	Ile	Leu	Asn	Phe	Asp	Leu	Asn	Tyr	Pro	325	330	335
Asn	Pro	Met	Asn	Phe	Leu	Arg	Arg	Ile	Ser	Lys	Ala	Asp	Asp	Tyr	Asp	340	345	350

Val Gln Ser Arg Thr Leu Gly Lys Tyr Leu Leu Glu Ile Thr Ile Val  
355 360 365

Asp Tyr Lys Phe Ile Gly Met Arg Pro Ser Leu Cys Cys Ala Leu Ala  
370 375 380

Met Tyr Leu Ala Arg Leu Ile Leu Gly Lys Leu Pro Val Trp Asn Gly  
385 390 395 400

Asn Leu Ile His Tyr Ser Gly Gly Tyr Arg Ile Ser Asp Met Arg Glu  
405 410 415

Cys Ile Glu Leu Met Phe Gln Tyr Leu Ile Ala Pro Ile Glu His Asp  
420 425 430

Glu Phe Phe Lys Lys Tyr Ala Met Arg Lys Phe Met Arg Ala Ser Thr  
435 440 445

Leu Cys Arg Asn Trp Ala Lys Lys Phe Gln Ala Ser Gly Arg Asp Leu  
450 455 460

Phe Asp Glu Arg Leu Ser Thr His Arg Leu Thr Leu Glu Asp Asp Asp  
465 470 475 480

Glu Glu Glu Glu Ile Val Val Ala Glu Ala Glu Glu  
485 490

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ser Thr Ala Ala Val Ala Thr Lys Pro Ser Val Thr Ser Lys Pro  
1 5 10 15

Ala Thr Lys Gln Val Leu Asn Tyr Thr Lys Glu Lys Lys Val Gly Glu  
20 25 30

Gly Thr Tyr Ala Val Val Tyr Leu Gly Lys Gln Ile Ser Thr Lys Arg  
35 40 45

Gln Ile Ala Ile Lys Glu Ile Lys Thr Gly Leu Phe Lys Asp Gly Leu  
50 55 60

Asp Met Ser Ala Leu Arg Glu Val Lys Tyr Leu Gln Glu Leu Lys His  
65 70 75 80

Pro Asn Val Ile Glu Leu Val Asp Val Phe Ser Ala Thr Asn Asn Leu  
85 90 95

Asn Leu Val Leu Glu Phe Leu Pro Cys Asp Leu Glu Val Leu Ile Lys  
100 105 110

Asp Lys Ser Ile Val Phe Lys Ser Ala Asp Ile Lys Ser Trp Leu Leu

115	120	125
Met Thr Leu Arg Gly Ile His His Cys His Arg Asn Phe Ile Leu His		
130	135	140
Arg Asp Leu Lys Pro Asn Asn Leu Leu Leu Ala Pro Asp Gly Gln Leu		
145	150	155
Lys Ile Ala Asp Phe Gly Leu Ala Arg Ala Leu Val Asn Pro Asn Glu		
	165	170
Asp Leu Ser Ser Asn Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu		
	180	185
Leu Phe Gly Ala Arg His Tyr Thr Gly Ala Val Asp Ile Trp Ser Ile		
	195	200
Gly Ile Ile Phe Ala Glu Leu Met Leu Arg Ile Pro Tyr Leu Pro Gly		
210	215	220
Lys Asp Asp Val Asp Gln Leu Asp Val Thr Phe Arg Ala Tyr Gly Thr		
225	230	235
Pro Thr Glu Gln Ile Trp Pro Asn Val Ser Ser Leu Pro Met Tyr Asn		
	245	250
Ala Leu His Val Tyr Pro Pro Pro Ser Arg Gln Glu Leu Arg Asn Arg		
	260	265
Phe Ser Ala Ala Thr Glu Lys Ala Leu Asp Leu Leu Ile Ser Met Thr		
	275	280
Gln Leu Asp Pro Ser Arg Arg Cys Asp Ser Thr Leu Ala Leu Leu His		
290	295	300
Asp Tyr Phe Thr Glu Ser Pro Arg Pro Thr Asp Pro Lys Lys Leu Pro		
305	310	315
Lys Lys Ser Ser Pro Glu Lys Arg Glu Asn Glu Asp Glu Gln Asn Asn		
	325	330
Gly Ser Lys Arg Arg His Val		
	340	

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Cys Ser Ala Ile Asp Thr Lys Ser Ser Val Ser Ala Met Glu His Lys
1 5 10 15
Ile Ala Ile Lys Lys Val Thr Lys Ile Phe Asn Lys Asp Ile Leu Leu
20 25 30
Ile Arg Ala Ile Arg Glu Leu Lys Phe Met Met Phe Phe Arg Gly His

	35		40		45	
Lys	Asn	Ile	Ala	Thr	Leu	Leu
	50				55	Asp
						Leu
						Asp
						Val
						Val
						Tyr
						Val
						Lys
						Pro
Tyr	Glu	Gly	Leu	Tyr	Cys	Phe
65					70	Gln
						Glu
						Leu
						Ala
						Asp
						Leu
						Asp
						Leu
						Ala
Arg	Val	Leu	Tyr	Ser	Asn	Val
				85		Gln
						Phe
						Ser
						Glu
						Phe
						His
						Ile
						Gln
						Ser
Phe	Met	Tyr	Gln	Ile	Leu	Cys
			100			Gly
						Leu
						Lys
						Tyr
						Ile
						His
						Ser
						Ala
						Asp
Val	Ile	His	Arg	Asp	Leu	Lys
		115				Pro
						Gly
						Asn
						Ile
						Leu
						Val
						Thr
						Thr
						Gln
Gly	Thr	Leu	Lys	Ile	Cys	Asp
	130					Phe
						Gly
						Leu
						Ala
						Arg
						Gly
						Ile
						Asn
						Pro
Val	Tyr	Phe	Arg	Asn	Arg	Ser
145					150	Ala
						Val
						Ile
						Thr
						Asn
						Tyr
						Val
						Ala

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1019 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1017

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG	AAG	TTG	TCA	GAT	TAT	TAT	ATA	GAC	AAG	GAA	TTA	ATT	TAC	AAT	AGT	48
Met	Lys	Leu	Ser	Asp	Tyr	Tyr	Ile	Asp	Lys	Glu	Leu	Ile	Tyr	Asn	Ser	
1				5				10						15		
GCC	ATT	TCT	GAT	ATA	TAT	ACG	GCT	ATT	GAT	AAG	TTT	AAT	AAC	TTA	CCA	96
Ala	Ile	Ser	Asp	Ile	Tyr	Thr	Ala	Ile	Asp	Lys	Phe	Asn	Asn	Leu	Pro	
			20				25						30			
GTA	TGT	CTT	AAA	ATA	GTT	GAT	GAA	GAT	TTC	AGT	CTT	CCA	CCA	CAT	TCA	144
Val	Cys	Leu	Lys	Ile	Val	Asp	Glu	Asp	Phe	Ser	Leu	Pro	Pro	His	Ser	
		35				40					45					
ATC	CAT	CGA	GAA	ATT	TTT	ATA	CTT	AAA	ACT	TTG	AAA	CCA	CAT	CCA	AAC	192
Ile	His	Arg	Glu	Ile	Phe	Ile	Leu	Lys	Thr	Leu	Lys	Pro	His	Pro	Asn	
	50					55				60						
ATA	ATT	GAA	TAT	TTT	AAT	GAT	CTT	AAA	ATT	TAT	GAT	GAT	GTT	ATA	TTA	240
Ile	Ile	Glu	Tyr	Phe	Asn	Asp	Leu	Lys	Ile	Tyr	Asp	Asp	Val	Ile	Leu	
65					70					75					80	

GTC	ACC	AAA	TTG	TAT	CGT	TAT	GAT	TTG	AGT	CAA	TTG	ATT	GAA	ATT	ACA	288
Val	Thr	Lys	Leu	Tyr	Arg	Tyr	Asp	Leu	Ser	Gln	Leu	Ile	Glu	Ile	Thr	
				85					90					95		
AAA	TAT	TGT	AAA	CGA	ACA	ACA	CGA	TTT	ATT	TAT	GGT	ATT	AAT	GGT	AAT	336
Lys	Tyr	Cys	Lys	Arg	Thr	Thr	Arg	Phe	Ile	Tyr	Gly	Ile	Asn	Gly	Asn	
			100					105					110			
CTT	GTT	AGT	AAT	CAA	TAT	ACA	CTT	GCT	AAT	GAA	ATT	GAA	GAA	AAA	GAT	384
Leu	Val	Ser	Asn	Gln	Tyr	Thr	Leu	Ala	Asn	Glu	Ile	Glu	Glu	Lys	Asp	
		115					120					125				
ATC	AAA	TTA	TGG	TTA	AAA	TCA	ATG	AGT	TCA	GGA	CTT	GAA	TTT	ATT	CAT	432
Ile	Lys	Leu	Trp	Leu	Lys	Ser	Met	Ser	Ser	Gly	Leu	Glu	Phe	Ile	His	
	130					135					140					
TCA	CAA	GGG	ATA	ATT	CAT	CGT	GAT	ATA	AAA	CCC	AGT	AAT	ATT	TTC	TTT	480
Ser	Gln	Gly	Ile	Ile	His	Arg	Asp	Ile	Lys	Pro	Ser	Asn	Ile	Phe	Phe	
145					150					155					160	
GCC	CGG	GAT	GAT	ATA	ACA	CAA	CCG	ATT	ATT	GGA	GAT	TTT	GAT	ATT	TGT	528
Ala	Arg	Asp	Asp	Ile	Thr	Gln	Pro	Ile	Ile	Gly	Asp	Phe	Asp	Ile	Cys	
				165				170						175		
TAT	GAT	TTA	AAA	CTG	CCA	CCT	AAA	GAT	GAA	CCC	CCT	ATG	GCG	AAA	TAT	576
Tyr	Asp	Leu	Lys	Leu	Pro	Pro	Lys	Asp	Glu	Pro	Pro	Met	Ala	Lys	Tyr	
			180				185						190			
ATT	GAT	GTA	TCT	ACA	GGT	ATT	TAT	AAA	GCA	CCA	GAA	TTG	ATT	CTT	GGT	624
Ile	Asp	Val	Ser	Thr	Gly	Ile	Tyr	Lys	Ala	Pro	Glu	Leu	Ile	Leu	Gly	
		195					200					205				
ATA	ACT	AAT	TAT	GAA	TAT	GAA	ATT	GAT	ATT	TGG	TCA	TTG	GGT	ATA	ATT	672
Ile	Thr	Asn	Tyr	Glu	Tyr	Glu	Ile	Asp	Ile	Trp	Ser	Leu	Gly	Ile	Ile	
	210					215					220					
TTG	ACT	GGT	TTA	TAT	TCA	GAA	AAT	TTT	CAA	AGT	GTT	TTA	GTC	AAA	GAT	720
Leu	Thr	Gly	Leu	Tyr	Ser	Glu	Asn	Phe	Gln	Ser	Val	Leu	Val	Lys	Asp	
225					230					235					240	
GAT	AAA	GAA	TTG	ACT	AAT	GAT	TCT	CAT	GTT	AGT	GAT	TTA	TAT	TTA	TTA	768
Asp	Lys	Glu	Leu	Thr	Asn	Asp	Ser	His	Val	Ser	Asp	Leu	Tyr	Leu	Leu	
				245				250						255		
AAT	CAA	ATA	TTT	GAA	AAT	TTC	GGT	ACA	CCC	AAT	TTA	ACT	GAT	TTT	GAA	816
Asn	Gln	Ile	Phe	Glu	Asn	Phe	Gly	Thr	Pro	Asn	Leu	Thr	Asp	Phe	Glu	
			260				265						270			
GAT	GAA	TTA	TTT	TGT	GAT	GAA	TAT	AAT	AAT	GAA	AAC	TTG	CAT	TTT	AAA	864
Asp	Glu	Leu	Phe	Cys	Asp	Glu	Tyr	Asn	Asn	Glu	Asn	Leu	His	Phe	Lys	
		275					280					285				
AAA	TTC	AAT	TTA	CAA	AAA	TAT	CCT	AGA	AAA	GAT	TGG	GAT	ATT	ATT	TTA	912
Lys	Phe	Asn	Leu	Gln	Lys	Tyr	Pro	Arg	Lys	Asp	Trp	Asp	Ile	Ile	Leu	
	290					295					300					
CCT	CGA	TGC	AAT	GAT	GAT	TTA	ATG	AAA	GAA	ATT	TTT	ACC	AAG	ATG	ATT	960
Pro	Arg	Cys	Asn	Asp	Asp	Leu	Met	Lys	Glu	Ile	Phe	Thr	Lys	Met	Ile	
305					310					315					320	
AGA	TAT	GAT	CGA	AGT	AAA	AGA	ATA	ACT	TCT	AAA	GAA	ATC	TTA	CAA	TTA	1008
Arg	Tyr	Asp	Arg	Ser	Lys	Arg	Ile	Thr	Ser	Lys	Glu	Ile	Leu	Gln	Leu	

60

325

330

335

ATG TTG GAT TG  
Met Leu Asp

1019

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Lys	Leu	Ser	Asp	Tyr	Tyr	Ile	Asp	Lys	Glu	Leu	Ile	Tyr	Asn	Ser	1	5	10	15
Ala	Ile	Ser	Asp	Ile	Tyr	Thr	Ala	Ile	Asp	Lys	Phe	Asn	Asn	Leu	Pro	20	25	30	
Val	Cys	Leu	Lys	Ile	Val	Asp	Glu	Asp	Phe	Ser	Leu	Pro	Pro	His	Ser	35	40	45	
Ile	His	Arg	Glu	Ile	Phe	Ile	Leu	Lys	Thr	Leu	Lys	Pro	His	Pro	Asn	50	55	60	
Ile	Ile	Glu	Tyr	Phe	Asn	Asp	Leu	Lys	Ile	Tyr	Asp	Asp	Val	Ile	Leu	65	70	75	80
Val	Thr	Lys	Leu	Tyr	Arg	Tyr	Asp	Leu	Ser	Gln	Leu	Ile	Glu	Ile	Thr	85	90	95	
Lys	Tyr	Cys	Lys	Arg	Thr	Thr	Arg	Phe	Ile	Tyr	Gly	Ile	Asn	Gly	Asn	100	105	110	
Leu	Val	Ser	Asn	Gln	Tyr	Thr	Leu	Ala	Asn	Glu	Ile	Glu	Glu	Lys	Asp	115	120	125	
Ile	Lys	Leu	Trp	Leu	Lys	Ser	Met	Ser	Ser	Gly	Leu	Glu	Phe	Ile	His	130	135	140	
Ser	Gln	Gly	Ile	Ile	His	Arg	Asp	Ile	Lys	Pro	Ser	Asn	Ile	Phe	Phe	145	150	155	160
Ala	Arg	Asp	Asp	Ile	Thr	Gln	Pro	Ile	Ile	Gly	Asp	Phe	Asp	Ile	Cys	165	170	175	
Tyr	Asp	Leu	Lys	Leu	Pro	Pro	Lys	Asp	Glu	Pro	Pro	Met	Ala	Lys	Tyr	180	185	190	
Ile	Asp	Val	Ser	Thr	Gly	Ile	Tyr	Lys	Ala	Pro	Glu	Leu	Ile	Leu	Gly	195	200	205	
Ile	Thr	Asn	Tyr	Glu	Tyr	Glu	Ile	Asp	Ile	Trp	Ser	Leu	Gly	Ile	Ile	210	215	220	
Leu	Thr	Gly	Leu	Tyr	Ser	Glu	Asn	Phe	Gln	Ser	Val	Leu	Val	Lys	Asp	225	230	235	240

[illegible]